

57528

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P4/09

#3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,975

DATE: 06/12/2001

TIME: 11:48:47

Input Set : A:\sequence.app

Output Set: N:\CRF3\06122001\I674975.raw

ENTERED

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3 <110> APPLICANT: Agus, David B.
4   Scheinberg, David
5   Zelenetz, Andrew D.
6   Roberts, Wendy
8 <120> TITLE OF INVENTION: Compositions and Methods for Active Vaccination
10 <130> FILE REFERENCE: MSKP039US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/674,975
C--> 13 <141> CURRENT FILING DATE: 2000-11-07
15 <150> PRIOR APPLICATION NUMBER: 60/084,870
16 <151> PRIOR FILING DATE: 1998-05-08
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 44
24 <212> TYPE: PRT
25 <213> ORGANISM: HUMAN
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28 <223> OTHER INFORMATION: human CD20 fragment
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35             20             25             30
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38             35             40
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46 <220> FEATURE:
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50 Thr Leu Ser His Phe Leu Lys Met Arg Arg Leu Glu Leu Ile Gln Thr
51   1             5             10             15
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54             20             25             30
56 Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Asn Ser
57             35             40
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63 <213> ORGANISM: HUMAN
65 <220> FEATURE:
66 <223> OTHER INFORMATION: exon VI of human CD20 gene
68 <400> SEQUENCE: 3
69 Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
70   1             5             10             15

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72 Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
73           20           25           30
75 His Phe Leu Lys His Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
76           35           40           45
78 Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
79           50           55           60
81 Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu
82 65           70           75
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86 <211> LENGTH: 237
87 <212> TYPE: DNA
88 <213> ORGANISM: HUMAN
90 <220> FEATURE:
91 <223> OTHER INFORMATION: exon VI of human CD20 gene
93 <400> SEQUENCE: 4
94 gtcaaaggaa aaatgataat gaattcattg agcctctttg ctgccatttc tggaaatgatt 60
95 ctttcaatca tggacatact taatattaaa atttccatt ttttaaaaat ggagagtctg 120
96 aattttatta gagtcacac accatatatt aacatataca actgtgaacc agctaattccc 180
97 tctgagaaaa actcccatc tacccaatac tgttacagca tacaatctct gttcttg 237
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102 <212> TYPE: PRT
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105 <220> FEATURE:
106 <223> OTHER INFORMATION: human Her2
108 <400> SEQUENCE: 5
109 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
110 1           5           10           15
112 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
113           20           25           30
115 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
116           35           40           45
118 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
119           50           55           60
121 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
122 65           70           75           80
124 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
125           85           90           95
127 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
128           100          105          110
130 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
131           115          120          125
133 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
134           130          135          140
136 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
137 145          150          155          160
139 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
140           165          170          175
142 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys

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143          180          185          190
145 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
146          195          200          205
148 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
149          210          215          220
151 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
152 225          230          235          240
154 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
155          245          250          255
157 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
158          260          265          270
160 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
161          275          280          285
163 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
164          290          295          300
166 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
167 305          310          315          320
169 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
170          325          330          335
172 Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
173          340          345          350
175 Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
176          355          360          365
178 Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
179          370          375          380
181 Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
182 385          390          395          400
184 Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
185          405          410          415
187 Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
188          420          425          430
190 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
191          435          440          445
193 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
194          450          455          460
196 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
197 465          470          475          480
199 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
200          485          490          495
202 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
203          500          505          510
205 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
206          515          520          525
208 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
209          530          535          540
211 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
212 545          550          555          560
214 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
215          565          570          575

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217 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
218          580          585          590
220 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
221          595          600          605
223 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
224          610          615          620
226 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
227 625          630          635          640
229 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
230          645          650          655
232 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
233          660          665          670
235 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
236          675          680          685
238 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
239          690          695          700
241 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
242 705          710          715          720
244 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
245          725          730          735
247 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
248          740          745          750
250 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
251          755          760          765
253 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
254          770          775          780
256 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
257 785          790          795          800
259 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
260          805          810          815
262 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
263          820          825          830
265 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
266          835          840          845
268 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
269          850          855          860
271 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
272 865          870          875          880
274 Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
275          885          890          895
277 Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
278          900          905          910
280 Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
281          915          920          925
283 Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
284          930          935          940
286 Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
287 945          950          955          960
289 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe

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290          965          970          975
292 Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
293          980          985          990
295 Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
296          995          1000          1005
298 Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
299          1010          1015          1020
301 Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
302          1025          1030          1035          1040
304 Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
305          1045          1050          1055
307 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
308          1060          1065          1070
310 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
311          1075          1080          1085
313 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
314          1090          1095          1100
316 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
317          1105          1110          1115          1120
319 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
320          1125          1130          1135
322 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
323          1140          1145          1150
325 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
326          1155          1160          1165
328 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
329          1170          1175          1180
331 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
332          1185          1190          1195          1200
334 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
335          1205          1210          1215
337 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
338          1220          1225          1230
340 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
341          1235          1240          1245
343 Leu Gly Leu Asp Val Pro Val
344          1250          1255
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348 <211> LENGTH: 1210
349 <212> TYPE: PRT
350 <213> ORGANISM: HUMAN
352 <220> FEATURE:
353 <223> OTHER INFORMATION: human EGFR
355 <400> SEQUENCE: 6
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360          20          25          30
362 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe

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VERIFICATION SUMMARY

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DATE: 06/12/2001

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Input Set : A:\sequence.app

Output Set: N:\CRF3\06122001\I674975.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date